

Patent Screen Results

Your Fasta Input (protein sequence):

>CL001165, SEQ ID NO:2, July 22, 2003

```
1  MAGTLDLDKG CTVEELLRGC IEAFDDSGKV RDPQLVRIFL MMHPWYIPSS
51 QLAAKLLHIY QQSRKDNSNS LQVKTCHLVR YWISAFPAEF DLNPELAEQI
101 KELKALLDQE GNRHSSLID IDSVPTYKWK RQVTQRNPVG QKKRKMSLLF
151 DHLEPMELAE HLTYLEYRSF CKILFQDYHS FVTHGCTVDN PVLERFISLF
201 NSVSQWVQLM ILSKPTAPQR ALVITHFVHV AEKLLQLQNF NTLMAVVGGL
251 SHSSISRLKE THSHVSPETI KLWEGLTEL V TATGNYGNYR RRLAACVGFR
301 FPILGVHLKD LVALQLALPD WLDPARTRLN GAKMKQLFSI LEELAMVTSL
351 RPPVQANPDL LSLTLVSLDQ YQTEDELYQL SLQREPRSKS SPTSPTSCTP
401 PPRPPVLEEW TSAAKPKLDQ ALVVEHIEKM VESVFRNFDV DGDGHISQEE
451 FQIIRGNFPY LSAFGDLDQN QDGCISREEM VSYFLRSSSV LGGRMGFVHN
501 FQESNSLRPV ACRHCKALIL GIYKQGLKCR ACGVNCHKQC KDRLSVECCR
551 RAQSVSLEGS APSPSPMHS HHRAFSFSLP RPGRRGSRPP AIPLPAEIRE
601 EEVQTVEDGV FDIHL
```

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= CL001165, SEQ ID NO:2, July 22, 2003
(615 letters)

Database: /work/eda3/blast/public/geneseqp_all.fasta
952,616 sequences; 143,563,330 total letters

| Sequences producing significant alignments: | Score (bits) | E Value |
|--|-----------------|------------|
| CRA 224000031063092 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 1261 | 0.0 |
| CRA 1000686599217 /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 1241 | 0.0 |
| CRA 1000686599217 /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 1241 | 0.0 |
| CRA 335001100361543 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 1241 | 0.0 |
| CRA 224000031063095 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 1241 | 0.0 |
| CRA 1000686599217 /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 1241 | 0.0 |
| CRA 1000748851985 /dataset=GENESEQ /org=Mus musculus /taxon=100... | 1202 | 0.0 |
| CRA 1000748851985 /dataset=GENESEQ /org=Mus musculus /taxon=100... | 1202 | 0.0 |
| CRA 224000031063098 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 618 | e-176 |
| CRA 223000007200244 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 589 | e-167 |
| CRA 1000686929020 /dataset=GENESEQ /org=Rattus norvegicus /taxo... | 526 | e-148 |
| CRA 224000031063100 /dataset=GENESEQ /org=Rattus norvegicus /ta... | 526 | e-148 |
| CRA 1000686929016 /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 520 | e-147 |
| CRA 225000034701186 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 467 | e-131 |
| CRA 223000007200081 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 274 | 1e-72 |
| CRA 32000240226777 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 196 | 4e-49 |
| CRA 32000240226777 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 196 | 4e-49 |
| CRA 32000240226777 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 196 | 4e-49 |
| CRA 32000240226777 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 196 | 4e-49 |
| CRA 224000006129088 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 152 | 9e-36 |

| | | |
|--|-----|-------|
| CRA 92000042379714 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 150 | 2e-35 |
| CRA 223000007205399 /dataset=GENESEQ /org=Synthetic /taxon=0 /m... | 126 | 4e-28 |
| CRA 223000007205399 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 126 | 4e-28 |
| CRA 63000081706862 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 104 | 2e-21 |
| CRA 224000006093606 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 103 | 4e-21 |
| CRA 1000685947861 /dataset=GENESEQ /org=Saccharomyces cerevisia... | 103 | 4e-21 |
| CRA 1000687166576 /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 103 | 4e-21 |
| CRA 1000686662576 /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 103 | 4e-21 |
| CRA 1000686399459 /dataset=GENESEQ /org=Saccharomyces cerevisia... | 98 | 2e-19 |
| CRA 224000006020317 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 96 | 5e-19 |
| CRA 223000036934911 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 96 | 5e-19 |
| CRA 1000686061280 /dataset=GENESEQ /org=Rattus norvegicus /taxo... | 96 | 5e-19 |
| CRA 1000685996049 /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 96 | 5e-19 |
| CRA 1000686061280 /dataset=GENESEQ /org=Rattus rattus /taxon=10... | 96 | 5e-19 |
| CRA 1000685985835 /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 96 | 5e-19 |
| CRA 335001099273961 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 96 | 5e-19 |
| CRA 335001099273784 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 96 | 5e-19 |
| CRA 1000685989171 /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 94 | 3e-18 |
| CRA 89000000250715 /dataset=GENESEQ /org=Drosophila melanogaste... | 92 | 1e-17 |
| CRA 89000000250718 /dataset=GENESEQ /org=Drosophila melanogaste... | 92 | 1e-17 |
| CRA 1000748845537 /dataset=GENESEQ /org=Mus musculus /taxon=100... | 92 | 1e-17 |
| CRA 225000034701200 /dataset=GENESEQ /org=Synthetic /taxon=0 /m... | 91 | 2e-17 |
| CRA 224000014674492 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 90 | 4e-17 |
| CRA 83000041216364 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 89 | 9e-17 |
| CRA 224000021583802 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 87 | 3e-16 |
| CRA 1000685968102 /dataset=GENESEQ /org=Schizosaccharomyces pom... | 87 | 4e-16 |
| CRA 89000000218737 /dataset=GENESEQ /org=Drosophila melanogaste... | 85 | 1e-15 |
| CRA 54000027878904 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 83 | 5e-15 |
| CRA 222000046172220 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 82 | 8e-15 |
| CRA 223000007205036 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 82 | 8e-15 |
| CRA 223000007205034 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 82 | 8e-15 |
| CRA 32000240222995 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 82 | 8e-15 |
| CRA 223000037392483 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 82 | 8e-15 |
| CRA 78000203049669 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 82 | 8e-15 |
| CRA 78000203047998 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 82 | 8e-15 |
| CRA 110000025777977 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 82 | 8e-15 |
| CRA 150000001907525 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 81 | 2e-14 |
| CRA 150000001907525 /dataset=GENESEQ /org=Mus sp /taxon=0 /mol_... | 81 | 2e-14 |
| CRA 335001101621173 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 80 | 3e-14 |
| CRA 63000081704667 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 80 | 3e-14 |
| CRA 335001101621173 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 80 | 3e-14 |
| CRA 92000042379710 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 80 | 4e-14 |
| CRA 78000202261506 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 79 | 7e-14 |
| CRA 335001101589911 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 79 | 1e-13 |
| CRA 89000000235742 /dataset=GENESEQ /org=Drosophila melanogaste... | 78 | 2e-13 |
| CRA 1000685797307 /dataset=GENESEQ /org=Drosophila melanogaster... | 77 | 4e-13 |
| CRA 335001099373653 /dataset=GENESEQ /org=Mus sp /taxon=0 /mol_... | 75 | 1e-12 |
| CRA 89000000249194 /dataset=GENESEQ /org=Drosophila melanogaste... | 73 | 7e-12 |
| CRA 224000021230274 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 72 | 9e-12 |
| CRA 32000240222108 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 71 | 2e-11 |
| CRA 32000240223064 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 71 | 2e-11 |
| CRA 32000240222108 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 71 | 2e-11 |
| CRA 100000004443992 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 71 | 2e-11 |
| CRA 224000006520423 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 71 | 3e-11 |
| CRA 216000000318831 /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 71 | 3e-11 |
| CRA 32000240223279 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 70 | 5e-11 |
| CRA 32000240223279 /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 70 | 5e-11 |

| | | | |
|---------------------|--|----|-------|
| CRA 335001099151798 | /dataset=GENESEQ /org=Mus musculus /taxon=1... | 69 | 6e-11 |
| CRA 335001099283708 | /dataset=GENESEQ /org=Mus musculus /taxon=1... | 69 | 6e-11 |
| CRA 335001099273788 | /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 69 | 6e-11 |
| CRA 335001101562668 | /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 69 | 8e-11 |
| CRA 114000033809387 | /dataset=GENESEQ /org=Rattus norvegicus /ta... | 69 | 1e-10 |
| CRA 119000051867519 | /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 69 | 1e-10 |
| CRA 335001099147156 | /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 68 | 2e-10 |
| CRA 225000014323451 | /dataset=GENESEQ /org=Aequorea victoria /ta... | 67 | 4e-10 |
| CRA 1000686946771 | /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 66 | 5e-10 |
| CRA 1000685997465 | /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 66 | 7e-10 |
| CRA 1000685997465 | /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 66 | 7e-10 |
| CRA 335001099273786 | /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 64 | 2e-09 |
| CRA 66000065726001 | /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 64 | 2e-09 |
| CRA 76000053367063 | /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 64 | 3e-09 |
| CRA 76000053367063 | /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 64 | 3e-09 |
| CRA 76000053367063 | /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 64 | 3e-09 |
| CRA 1000686652278 | /dataset=GENESEQ /org=Homo sapiens /taxon=960... | 64 | 3e-09 |
| CRA 76000053367063 | /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 64 | 3e-09 |
| CRA 76000053367063 | /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 64 | 3e-09 |
| CRA 76000053367063 | /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 64 | 3e-09 |
| CRA 76000053367063 | /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 64 | 3e-09 |
| CRA 89000000250454 | /dataset=GENESEQ /org=Drosophila melanogaste... | 64 | 4e-09 |
| CRA 335001100395205 | /dataset=GENESEQ /org=Rattus sp /taxon=0 /m... | 64 | 4e-09 |
| CRA 32000240223033 | /dataset=GENESEQ /org=Homo sapiens /taxon=96... | 64 | 4e-09 |
| CRA 105000014693956 | /dataset=GENESEQ /org=Drosophila melanogast... | 63 | 6e-09 |
| CRA 335001099151800 | /dataset=GENESEQ /org=Mus musculus /taxon=1... | 63 | 6e-09 |
| CRA 103000001533731 | /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 63 | 6e-09 |
| CRA 103000001533731 | /dataset=GENESEQ /org=Homo sapiens /taxon=9... | 63 | 6e-09 |
| CRA 89000000234368 | /dataset=GENESEQ /org=Drosophila melanogaste... | 62 | 8e-09 |

```

>CRA|224000031063092 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
    /mol_type=aa /date=16-JAN-03 /length=615
    /altid=derwent_ac|AA026354 /altid=derwent_id|AA026354
    /def=Human Ras-like protein /patent=WO200272765-A2
    /pat_section=Claim
    Length = 615

```

Score = 1261 bits (3226), Expect = 0.0
Identities = 615/615 (100%), Positives = 615/615 (100%)

```

Query: 1  MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
          MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY
Sbjct: 1  MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60

Query: 61  QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120
          QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID
Sbjct: 61  QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120

Query: 121  IDSVPTYKWKQRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
          IDSVPTYKWKQRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
Sbjct: 121  IDSVPTYKWKQRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Query: 181  FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240
          FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF
Sbjct: 181  FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240

Query: 241  NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300

```

NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR
 Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300

Query: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL 360
 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL
 Sbjct: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL 360

Query: 361 LSLTIVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420
 LSLTIVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ
 Sbjct: 361 LSLTIVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420

Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480
 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM
 Sbjct: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
 Sbjct: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHHHRAFSFSLPRPGRGRSRPPAIPPLAEIRE 600
 KDRLSVECRRAQSVSLEGSAPSPSPMHHHRAFSFSLPRPGRGRSRPPAIPPLAEIRE
 Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHHHRAFSFSLPRPGRGRSRPPAIPPLAEIRE 600

Query: 601 EEVQTVEDGVFDIHL 615
 EEVQTVEDGVFDIHL
 Sbjct: 601 EEVQTVEDGVFDIHL 615

>CRA|1000686599217 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
 /mol_type=aa /date=09-AUG-00 /length=609
 /altid=derwent_ac|AA70961 /altid=derwent_id|AA70961
 /def=Human Ras signalling pathway associated protein
 CalDAG-GEFI /patent=WO200024768-A2 /pat_section=Claim
 Length = 609

Score = 1241 bits (3176), Expect = 0.0
 Identities = 608/615 (98%), Positives = 609/615 (98%), Gaps = 6/615 (0%)

Query: 1 MAGTLDLDKGCTVEELLRGCI EAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
 MAGTLDLDKGCTVEELLRGCI EAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIY
 Sbjct: 1 MAGTLDLDKGCTVEELLRGCI EAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 60

Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120
 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID
 Sbjct: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120

Query: 121 IDSVPTYKWKQVTRQNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
 IDSVPTYKWKQVTRQNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
 Sbjct: 121 IDSVPTYKWKQVTRQNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240
 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF
 Sbjct: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240

Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300
 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR
 Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300

Query: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360
 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL
 Sbjct: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360

Query: 361 LSLTIVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420
 LSLTIVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ
 Sbjct: 361 LSLTIVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420

Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480
 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM
 Sbjct: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
 Sbjct: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHHHRAFSFSLPRPGRGRSRPPAIPLP AEIRE 600
 KDRLSVECRRAQSVSLEGSAPSPSPMHHHRAFSFSLPRPGRGRSRPP EIRE
 Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHHHRAFSFSLPRPGRGRSRPP-----EIRE 594

Query: 601 EEVQTVEDGVFDIHL 615
 EEVQTVEDGVFDIHL
 Sbjct: 595 EEVQTVEDGVFDIHL 609

>CRA|1000686599217 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
 /mol_type=aa /date=15-APR-99 /length=609
 /altid=derwent_ac|AAW87995 /altid=derwent_id|AAW87995
 /def=An alternatively spliced human MCG7 protein
 /patent=W09853061-A1 /pat_section=Claim
 Length = 609

Score = 1241 bits (3176), Expect = 0.0
 Identities = 608/615 (98%), Positives = 609/615 (98%), Gaps = 6/615 (0%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIY
 Sbjct: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 60

Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120
 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID
 Sbjct: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120

Query: 121 IDSVPTYKWKQRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
 IDSVPTYKWKQRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
 Sbjct: 121 IDSVPTYKWKQRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240
 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF
 Sbjct: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240

Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300
 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR
 Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300

Query: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360

Sbjct: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL 360
 Query: 361 LSLTIVSLDQYQTEDELYQLSLQREPRSKSSPTSPTCTPPPRPPVLEEWTSAAKPKLDQ 420
 LSLTIVSLDQYQTEDELYQLSLQREPRSKSSPTSPTCTPPPRPPVLEEWTSAAKPKLDQ
 Sbjct: 361 LSLTIVSLDQYQTEDELYQLSLQREPRSKSSPTSPTCTPPPRPPVLEEWTSAAKPKLDQ 420
 Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480
 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM
 Sbjct: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480
 Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
 Sbjct: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
 Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPPLPAEIRE 600
 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP EIRE
 Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP-----EIRE 594
 Query: 601 EEVQTVEDGVFDIHL 615
 EEVQTVEDGVFDIHL
 Sbjct: 595 EEVQTVEDGVFDIHL 609

>CRA|335001100361543 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
 /mol_type=aa /date=15-APR-99 /length=728
 /altid=derwent_ac|AAW87994 /altid=derwent_id|AAW87994
 /def=A human MCG7 protein /patent=W09853061-A1
 /pat_section=Claim
 Length = 728

Score = 1241 bits (3176), Expect = 0.0
 Identities = 608/615 (98%), Positives = 609/615 (98%), Gaps = 6/615 (0%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIY
 Sbjct: 120 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 179
 Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID 120
 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID
 Sbjct: 180 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID 239
 Query: 121 IDSVPTYKWKQVQVTRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
 IDSVPTYKWKQVQVTRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
 Sbjct: 240 IDSVPTYKWKQVQVTRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 299
 Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF 240
 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF
 Sbjct: 300 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF 359
 Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 300
 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR
 Sbjct: 360 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 419
 Query: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL 360
 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL
 Sbjct: 420 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL 479

Query: 361 LSLTLVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420
 LSLTLVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ
 Sbjct: 480 LSLTLVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 539

Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480
 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM
 Sbjct: 540 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 599

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
 Sbjct: 600 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 659

Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPPAEIRE 600
 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP EIRE
 Sbjct: 660 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP-----EIRE 713

Query: 601 EEVQTVEDGVFDIHL 615
 EEVQTVEDGVFDIHL
 Sbjct: 714 EEVQTVEDGVFDIHL 728

>CRA|224000031063095 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
 /mol_type=aa /date=16-JAN-03 /length=664
 /altid=derwent_ac|AAO26356 /altid=derwent_id|AAO26356
 /def=Ras-like related human protein, SEQ ID No 5
 /patent=WO200272765-A2 /pat_section=Disclosure;
 Length = 664

Score = 1241 bits (3176), Expect = 0.0
 Identities = 608/615 (98%), Positives = 609/615 (98%), Gaps = 6/615 (0%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIY
 Sbjct: 56 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 115

Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID 120
 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID
 Sbjct: 116 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID 175

Query: 121 IDSVPTYKWKQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
 IDSVPTYKWKQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
 Sbjct: 176 IDSVPTYKWKQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 235

Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240
 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF
 Sbjct: 236 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 295

Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 300
 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR
 Sbjct: 296 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 355

Query: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360
 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL
 Sbjct: 356 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 415

Query: 361 LSLTLVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420

LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ
 Sbjct: 416 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 475
 Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480
 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM
 Sbjct: 476 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 535
 Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
 Sbjct: 536 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 595
 Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPPLAEIRE 600
 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP EIRE
 Sbjct: 596 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP-----EIRE 649
 Query: 601 EEVQTVEDGVFDIHL 615
 EEVQTVEDGVFDIHL
 Sbjct: 650 EEVQTVEDGVFDIHL 664

>CRA|1000686599217 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
 /mol_type=aa /date=16-JAN-03 /length=609
 /altid=derwent_ac|AA026355 /altid=derwent_id|AA026355
 /def=Ras-like related human protein, SEQ ID No 4
 /patent=WO200272765-A2 /pat_section=Disclosure;
 Length = 609

Score = 1241 bits (3176), Expect = 0.0
 Identities = 608/615 (98%), Positives = 609/615 (98%), Gaps = 6/615 (0%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIY
 Sbjct: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 60
 Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID 120
 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID
 Sbjct: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID 120
 Query: 121 IDSVPTYKWKQVQVRNPVVGQKKRKMSSLFDHLEPMELAEHLTYEYRSFCKILFQDYHS 180
 IDSVPTYKWKQVQVRNPVVGQKKRKMSSLFDHLEPMELAEHLTYEYRSFCKILFQDYHS
 Sbjct: 121 IDSVPTYKWKQVQVRNPVVGQKKRKMSSLFDHLEPMELAEHLTYEYRSFCKILFQDYHS 180
 Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240
 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF
 Sbjct: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240
 Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 300
 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR
 Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 300
 Query: 301 FPILGVHLKDLVALQALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL 360
 FPILGVHLKDLVALQALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL
 Sbjct: 301 FPILGVHLKDLVALQALPDWLDPARTRLNGAKMKQLFSILEELAMVTSRPPVQANPDL 360
 Query: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420
 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ
 Sbjct: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420

Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480
 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM
 Sbjct: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
 Sbjct: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHRAFSFSLPRPGRGSRPPAIPPAEIRE 600
 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHRAFSFSLPRPGRGSRPP EIRE
 Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHRAFSFSLPRPGRGSRPP-----EIRE 594

Query: 601 EEVQTVEDGVFDIHL 615
 EEVQTVEDGVFDIHL
 Sbjct: 595 EEVQTVEDGVFDIHL 609

>CRA|1000748851985 /dataset=GENESEQ /org=Mus musculus /taxon=10090
 /mol_type=aa /date=09-AUG-00 /length=608
 /altid=derwent_ac|AAY70960 /altid=derwent_id|AAY70960
 /def=Mouse Ras signalling pathway associated protein
 CalDAG-GEFI /patent=WO200024768-A2 /pat_section=Claim
 Length = 608

Score = 1202 bits (3076), Expect = 0.0
 Identities = 589/615 (95%), Positives = 597/615 (96%), Gaps = 7/615 (1%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
 MA TLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLA+KLLH Y
 Sbjct: 1 MASTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLASKLLH FY 60

Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNP ELAEQIKELKALLDQEGNRRHSSLID 120
 QQSRKDNSNSLQVKTCHLVRYW+SAFPAEFDLNP ELAE IKELKALLDQEGNRRHSSLID
 Sbjct: 61 QQSRKDNSNSLQVKTCHLVRYWVSAPPAEFDLNP ELAEPIKELKALLDQEGNRRHSSLID 120

Query: 121 IDSVPTYKWK RQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
 I+SVPTYKWK RQVTQRNPV QKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
 Sbjct: 121 IESVPTYKWK RQVTQRNPVEQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQ RALVITHFVHVAEKLLQLQNF 240
 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTA Q RALVITHFVHVAEKLLQLQNF
 Sbjct: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTATQ RALVITHFVHVAEKLLQLQNF 240

Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGN YRRRLAACVGFR 300
 NTLMAVVGGLSHSSISRLKETHSHVSP+TIKLWEGLTELVTATGNY NYRRRLAACVGFR
 Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPDTIKLWEGLTELVTATGNYSNYRRRLAACVGFR 300

Query: 301 FPILGVHLKDLVALQLALPDWLD PARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360
 FPILGVHLKDLVALQLALPDWLD P RTRLNGAKM+QLFSILEELAMVTSLRPPVQANPDL
 Sbjct: 301 FPILGVHLKDLVALQLALPDWLD PGRTRLNGAKMRQLFSILEELAMVTSLRPPVQANPDL 360

Query: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420
 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTS AKPKLDQ
 Sbjct: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSVAKPKLDQ 420

Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480

ALV EHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM
Sbjct: 421 ALVAEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
+SYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
Sbjct: 481 ISYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHHRAFSFSLPRPGRRGSRPPAIPLP AEIRE 600
KDRLSVECRRAQSVSLEGSAPSPSP H+ HHRAFSFSLPRPGRR SRPP EIRE
Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSP THT-HHRAFSFSLPRPGRRSSRPP-----EIRE 593

Query: 601 EEVQTVEDGVFDIHL 615
EEVQTVEDGVFDIHL
Sbjct: 594 EEVQTVEDGVFDIHL 608

>CRA|1000748851985 /dataset=GENESEQ /org=Mus musculus /taxon=10090
/mol_type=aa /date=16-JAN-03 /length=608
/altid=derwent_ac|AAO26357 /altid=derwent_id|AAO26357
/def=Ras-like related mouse protein, SEQ ID No 6
/patent=WO200272765-A2 /pat_section=Disclosure;
Length = 608

Score = 1202 bits (3076), Expect = 0.0
Identities = 589/615 (96%), Positives = 597/615 (96%), Gaps = 7/615 (1%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
MA TLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLA+KLLH Y
Sbjct: 1 MASTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLASKLLHIFY 60

Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNP ELAEQIKELKALLDQEGNRRHSSLID 120
QQSRKDNSNSLQVKTCHLVRYW+SAFPAEFDLNP ELAE IKELKALLDQEGNRRHSSLID
Sbjct: 61 QQSRKDNSNSLQVKTCHLVRYWVSAPPAEFDLNP ELAEPIKELKALLDQEGNRRHSSLID 120

Query: 121 IDSVPPTYKWKQVQTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
I+SVPTYKWKQVQTQRNPV QKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
Sbjct: 121 IESVPPTYKWKQVQTQRNPVEQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF 240
FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTA QRALVITHFVHVAEKLQLQNF
Sbjct: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTATQRALVITHFVHVAEKLQLQNF 240

Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 300
NTLMAVVGGLSHSSISRLKETHSHVSP+TIKLWEGLTELVTATGNY NYRRRLAACVGFR
Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPDTIKLWEGLTELVTATGNYSNYRRRLAACVGFR 300

Query: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360
FPILGVHLKDLVALQLALPDWLDP RTRLNGAKM+QLFSILEELAMVTSLRPPVQANPDL
Sbjct: 301 FPILGVHLKDLVALQLALPDWLDPGRTRLNGAKMRQLFSILEELAMVTSLRPPVQANPDL 360

Query: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420
LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTS AKPKLDQ
Sbjct: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSVAKPKLDQ 420

Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480
ALV EHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM
Sbjct: 421 ALVAEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
+SYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
Sbjct: 481 ISYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHRAFSFSLPRPGRRGSRPPAIPPLPAEIRE 600
KDRLSVECRRAQSVSLEGSAPSPSP H+ HHRAFSFSLPRPGRR SRPP EIRE
Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSPHTT-HHRAFSFSLPRPGRRSSRPP-----EIRE 593

Query: 601 EEVQTVEDGVFDIHL 615
EEVQTVEDGVFDIHL
Sbjct: 594 EEVQTVEDGVFDIHL 608

Database: /work/eda3/blast/public/geneseqp_all.fasta
Posted date: Mar 2, 2003 3:26 AM
Number of letters in database: 143,563,330
Number of sequences in database: 952,616

| Lambda | K | H |
|--------|-------|-------|
| 0.321 | 0.136 | 0.410 |

Gapped

| Lambda | K | H |
|--------|--------|-------|
| 0.270 | 0.0470 | 0.230 |

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 185709453
Number of Sequences: 952616
Number of extensions: 7789331
Number of successful extensions: 34968
Number of sequences better than 1.0e-08: 106
Number of HSP's better than 0.0 without gapping: 58
Number of HSP's successfully gapped in prelim test: 48
Number of HSP's that attempted gapping in prelim test: 34702
Number of HSP's gapped (non-prelim): 171
length of query: 615
length of database: 143,563,330
effective HSP length: 55
effective length of query: 560
effective length of database: 91,169,450
effective search space: 51054892000
effective search space used: 51054892000
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (21.9 bits)
S2: 149 (62.5 bits)